

PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

NOV 05 2004

In re Application of

Examiner: Slobodyansky, E.

MARCIREAU ET AL

Art Unit: 1652

Serial No.: **09/744,125**

Filed: September 17, 2001

hereby certify that this correspondence is being transmitted via facsimile to the Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, care of Art Unit 1640, (703) 305-3014 on

Title: MEKKI-INTERACTING FHA PROTEIN

Date of Deposit

Christophe Marcireau
Printed Name of Person Signing Certificate

Signature

DECLARATION UNDER 37 CFR § 1.131 OF PRIOR INVENTION IN A WORLD TRADE ORGANIZATION (WTO) MEMBER COUNTRY

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313

Dear Sir:

Christophe Marcireau declares as follows:

1. I am an inventor of the inventions claimed in U.S. Patent Application Serial No. 09/744,125 filed on September 17, 2001 ("the '125 application").
2. Prior to September 10, 1997 I obtained the nucleic acid of SEQ ID NO:1 in France, a WTO member country.
3. Prior to September 10, 1997, I translated SEQ ID NO:1 and obtained the amino acid sequence of SEQ ID NO:2 in France, a WTO member country.
4. Attached hereto is a machine-generated graph that shows the results of the sequencing of the nucleic acid of SEQ ID NO:1. The sequencing of SEQ ID

NO:1 and its translation to obtain the amino acid sequence of SEQ ID NO:2 was performed under my direction. The machine-generated date on the graph has been redacted, but that date is prior to September 10, 1997. The sequencing was conducted in France, a WTO member country.

5. I declare that all of the foregoing statements are true, recognizing that willful false statements are punishable by fine or imprisonment, or both, under 18 U.S.C. § 1001, and that any such willful false statements may jeopardize the validity of the application or any patent that issues from it.

Date: October the 12th


Christophe Marcireau

mbp3nt [1 to 1257] -> 1-phase Translation

DNA sequence 1603 b.p. GTGGATCCCCCG ... TCGCCCTATAGT linear

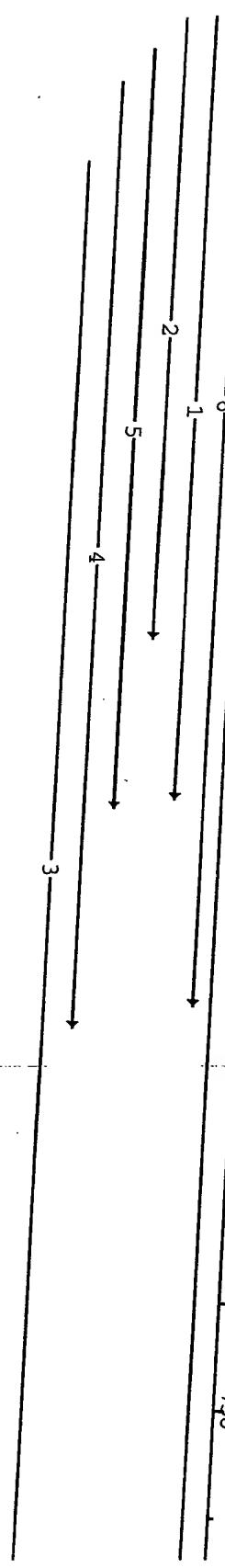
4909+8855+8855+6196 mekk1bp3

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 V D P P G C R N S A R G G V E P G R C S
 61/21 91/31
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 G S E P S S S E K K K V S K A P S T P V
 121/41 151/51
 CCA CCC AGC CCA GCC CCA GCC CCT GGA CTC ACC AAG CGT GTG AAg AAg AGT AAA CAG CCA
 P P S P A P A P G L T K R V K K S K Q P
 181/61 211/71
 CTT CAG GTG ACC AAG GAT CTG GGC CGC TGG AAg CCT GCA AAT GAC CTC CTG CTC ATA AAT
 L Q V T K D L G R W K P A N D L L L I N
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 421/141 451/151
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 K A L F S K A E E Q L L S K V G S T S Q
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 P T L E T F Q D L L H R H P D A F Y L A
 541/181 571/191
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 601/201 631/211
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 D Q T V Q P L P K G D Q V L N F S D A E
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 721/241 751/251
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 M V A D R R Q K R E I R Q L E Q E L H K
 781/261 811/271
 TGG CAG GTG CTA GTG GAC AGC ATC ACA GGC ATG AGC TCT CCG GAC TTC GAC AAC CAG ACA
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 GGC AGA GCA ACC AAG GAT AAC CAG ATT GAT GTG GAC CTG TCT CTG GAG GGT CCG GCC TGG
 G R A T K D N Q I D V D L S L E G P A W
 961/321 991/331
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 1021/341 1051/351
 AAT GAG GGT CGA CGG CCC ATC TAC ATC GAT GGA CGG CGG GTG CTC TGT GGC TCC AAA TGG
 N E G R R P I Y I D G R P V L C G S K W
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 Q D L I A L I R A E L P R S H H S E E W
 1201/401 1231/411
 TGG CAG GAC TCG TGG GCC CTC TCC GGC CTG TTT CCC CTG CCA CTC CAG CCC CCT TGA
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Ass EST

Page 1

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500
750



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Last assembled: [REDACTED]

16:09:01

16:09:55

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Total in assemblages:	6	2576	100.0%
Total unassembled:	0	0	0.0%
Total dye primer:	0	0	0.0%
Total dye terminator:	0	0	0.0%
Non-373 sequences:	6	2666	103.5%

	Sequences	Bases	Score	Ambiguities
w26888.Assemblage.1	6	831	1773.0	34

w26888.Assemblage.1	Sequences:	6	Bases:	831	Score: 1773.0
Redundancy	Average:	3.2	High:	6	Low: 1
Sequence Lengths	Average:	429	High:	640	Low: 282

File	Sample	ID	Begin	End	Length	Date	Chemistry
w26888		-> 6	0	562	535	12/03/97	
aa134651		-> 1	103	467	352	12/03/97	
f12127		-> 2	104	392	282	12/03/97	
w00383		-> 5	119	472	347	12/03/97	
t66207		-> 4	135	575	420	12/03/97	
r52839		-> 3	172	831	640	12/03/97	

Unassembled Sequences	Sequences:	0	Bases:	0			
File	Sample	ID	Begin	End	Length	Date	Chemistry

S1 mps Hs

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12127 J00383	250. 275. 300. 325. 350.
65207 573839	

untitled 2

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t5 2839 -> GAGCTGGTGGAGGAGCCGGTGGCAAAATCTTCTT-ACCCGGGCAAGGGGGCCAGT-GGGTAGTGGAAACCCCTCC-TCCAGTGAAAGAAGGTATT

\26888_Assembly.1 CAAAGCCCCCAGCCACTCTGTGCCACCCAGCCCAGGGATTCAACAGGTGAAAGATAACGCCATTTCAGGTGAACCAAGGATCTGGGGCGTTGGAA
650
675
700

-> CAAAGCCCCCAGCACTCTGTGCCACCCAGCCCAGCCAGGGATTCACCAAGCGTGTGAAGAAGAGTAAACAGCCATTTCAGGTGAACTTTTCTCCCCCTCCCCCTCCAAA
:52839

v26888 .Assembly.1 GCTTGCAATTGANCCTCTTATTAAATTGTTGAGCCAAACGACTTAACCTTACTTGTGTTACGTTAACCTTGGAAAGTTGAG

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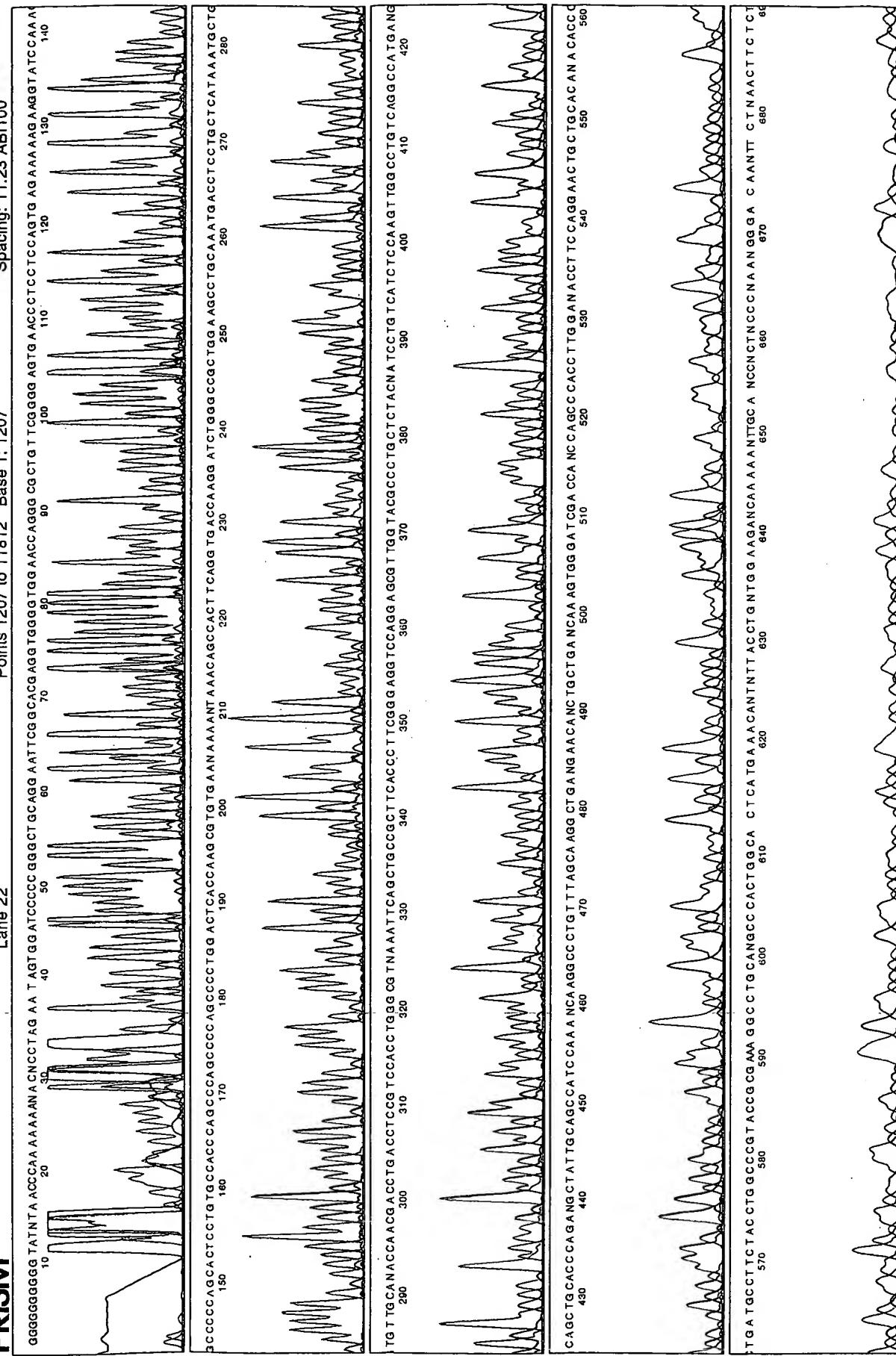


Model 377
Version 2.1.1

22-CM 5

Signal G:406 A:809 T:268 C:303
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Page 1 of 2



mbp3nt [1 to 1257] -> 1-phase Translation

DNA sequence 1603 b.p. GTGGATCCCCCG ... TCGCCCTATAGT linear

4909+8855+8955+8856+6196 mekk1bp3

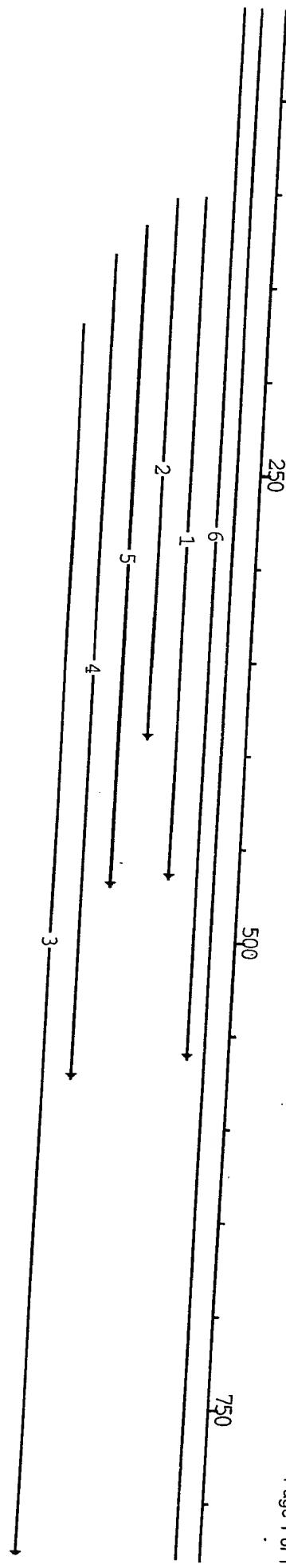
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 241/81 271/91
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 A V L Q T N D L T S V H L G V K F S C R
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 TTC ACC CTT CCG GAG GTC CAG GAG CGT TGG TAC GCC CTG CTC TAC gAT CCT GTC ATC TCC
 F T L R E V Q E R W Y A L L Y D P V I S
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 K A L F S K A E E Q L L S K V G S T S Q
 481/161 511/171
 CCC ACC TTG GAG ACC TTC CAG GAC CTG CTG CAC AGA CAC CCT GAT GCC TTC TAC CTG GCC
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 541/181 571/191
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 601/201 631/211
 GAC CAG ACA GTG CAG CCG CTG CCC AAA GGG GAC CAA GTG CTG AAC TTC TCT GAT GCA GAG
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 661/221 691/231
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 721/241 751/251
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 M V A D R R Q K R E I R Q L E Q E L H K
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 TGG CAG CTG CTA GTG GAC AGC ATC ACA GGC ATG AGC TCT CCG GAC TTC GAC AAC CAG ACA
 W Q V L V D S I T G M S S P D F D N Q T
 841/281 871/291
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 L A V L R G R M V R Y L M R S R E I T L
 901/301 931/311
 GGC AGA GCA ACC AAG GAT AAC CAG ATT GAT GTG GAC CTG TCT CTG GAG GGT CCG GCC TGG
 G R A T K D N Q I D V D L S L E G P A W
 961/321 991/331
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 K I S R K Q G V I K L K N N G D F F I A
 1021/341 1051/351
 AAT GAG GGT CGA CGG CCC ATC TAC ATC GAT GGA CGG CCG GTG CTC TGT GGC TCC AAA TGG
 N E G R R P I Y I D G R P V L C G S K W
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 R L S N N S V V E I A S L R F V F L I N
 1141/381 1171/391
 CAG GAC CTC ATT GCC CTC ATC AGG GCT GAG CTG CCA AGA TCA CAC CAC AGT GAG GAA TGG
 Q D L I A L I R A E L P R S H H S E E W
 1201/401 1231/411
 TGG CAG GAC TCG TGG GCC CTC TCC GGC CTG TTT CCC CTG CCA CTC CAG CCC CCT TGA
 W Q D S W A L S G L F P L P L Q P P *

Ass EST

Page 1 of 1

250
500
750

6
5
4
3
2
1



Project: Ass EST
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Last assembled: [REDACTED] 16:09:55

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Window: 13 Offset: 0 Tolerance: 1 Hit Count: 10 Overlap: 10%

	Sequences	Bases	Percent
Total in project:	6	2576	100.0%
Total in assemblages:	6	2576	100.0%
Total unassembled:	0	0	0.0%
Total dye primer:	0	0	0.0%
Total dye terminator:	0	0	0.0%
Non-373 sequences:	6	2666	103.5%

	Sequences	Bases	Score	Ambiguities
w26888.Assemblage.1	6	831	1773.0	34

w26888.Assemblage.1 Sequences: 6 Bases: 831 Score: 1773.0
Redundancy Average: 3.2 High: 6 Low: 1
Sequence Lengths Average: 429 High: 640 Low: 282

File	Sample	ID	Begin	End	Length	Date	Chemistry
w26888		-> 6	0	562	535	12/03/97	
aa134651		-> 1	103	467	352	12/03/97	
f12127		-> 2	104	392	282	12/03/97	
w00383		-> 5	119	472	347	12/03/97	
t66207		-> 4	135	575	420	12/03/97	
r52839		-> 3	172	831	640	12/03/97	

Unassembled Sequences File	Sample	Sequences:	0	Bases:	0	Length	Date	Chemistry
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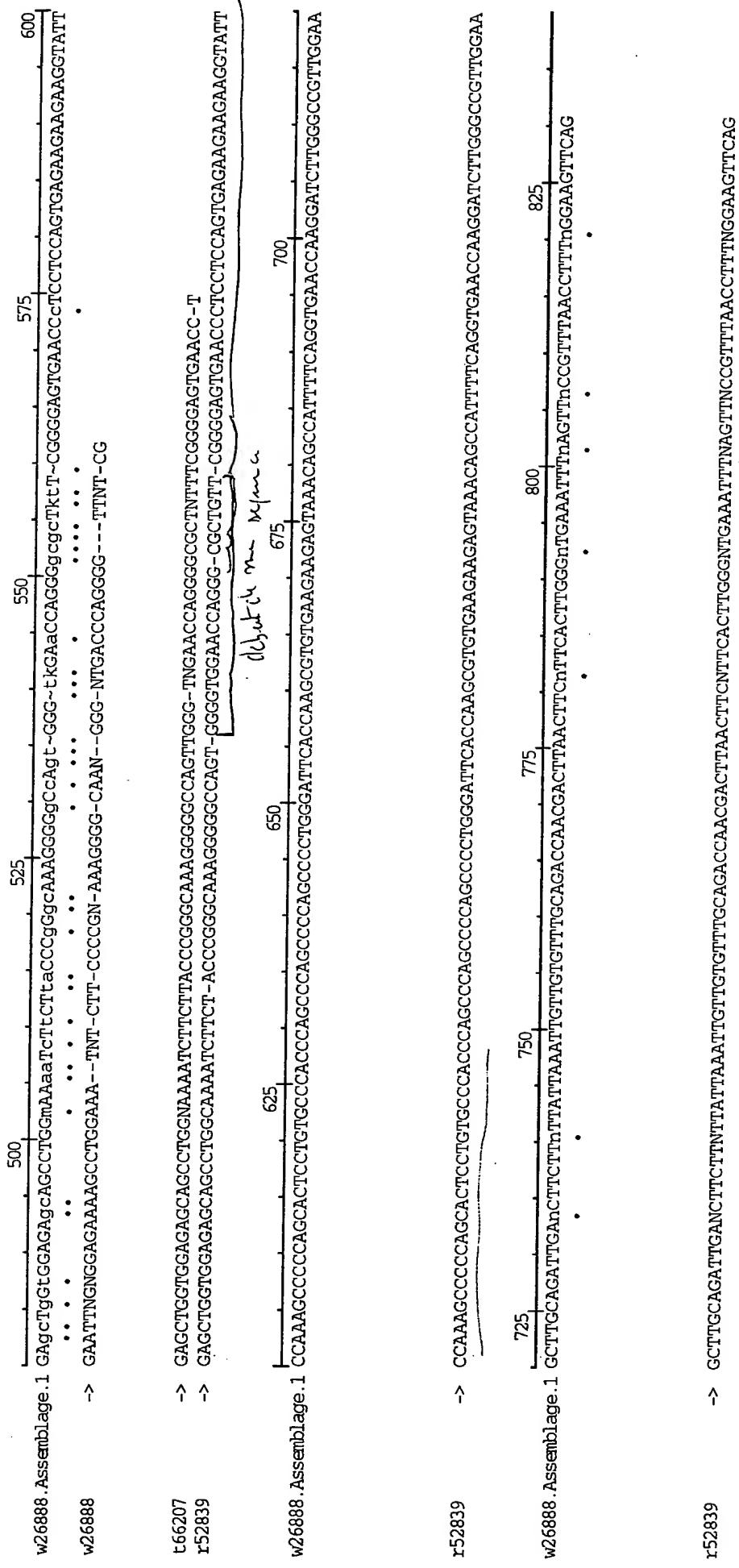
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Untitled?

Applied Biosystems

AutoAssembler™ 1.4.0

Page 1 of 2.

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 aa134651 → AGCGAAGCCGGCTTT-G
 f12127 → CGGAAGCCGNNCTTTTG
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ABI
PRISM

Model 377
Version 3.0
ABI100
Version 3.0

09.CM

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Lan
•60

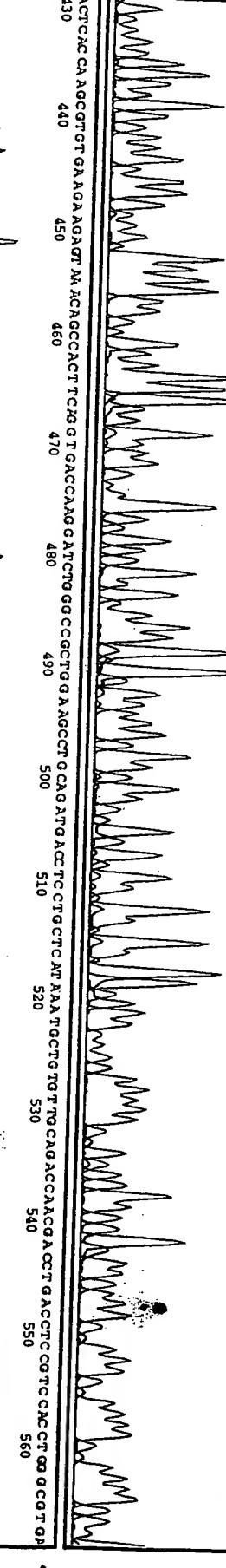
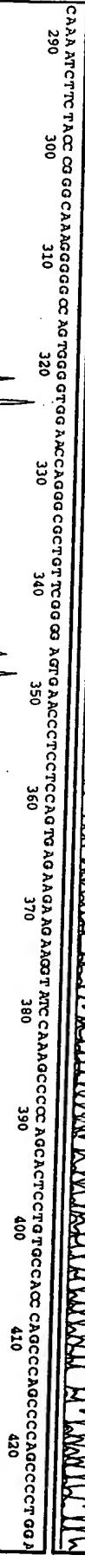
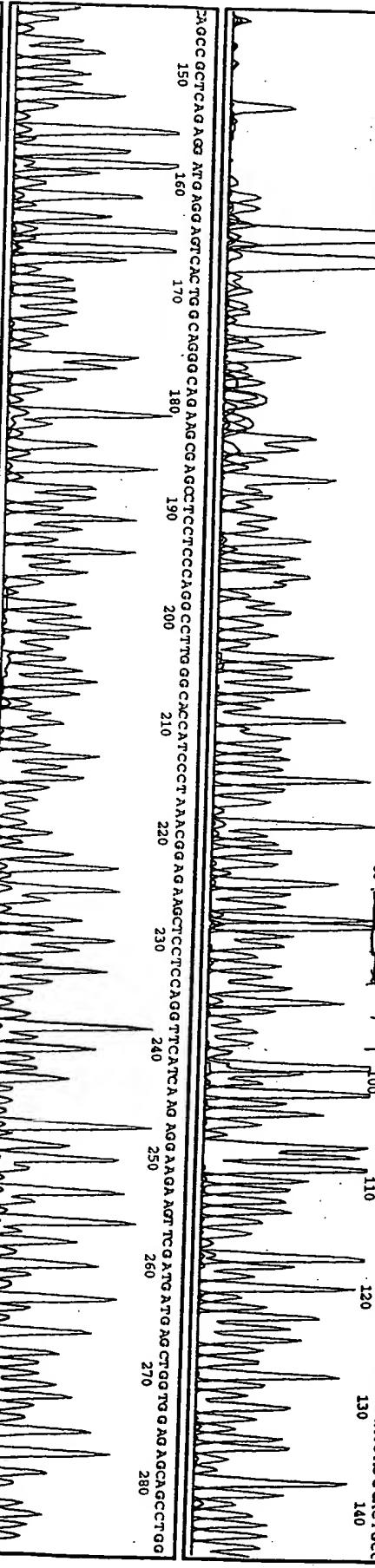
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Signal G:104 A:318 T:111 C:113
DT4%Ac{A Set-AnyPrimer}
SN 95080645

Page 1 of 2

points 1006 to 1188 Base 1: 1006

Spacing: 11.18{11.18}



... T C G C T A C C G C T T C C C C T T C G G A G T C C A G A N C G T T G G T A C C C T G C T C T A C G A T C C T G T C A T C T C C A A N T T G G C C T G T C A G G C A T G A A G C A G C T G C A C C C A N A A G C T N T T G C A G C A T C C A G A

The logo for ABI PRISM, featuring the word "ABI" stacked above "PRISM" in a bold, sans-serif font. A stylized DNA helix graphic is positioned between the two words.

Model 377
Version 3.0
ABI100
Version 3.0

Model 377
Version 3.0

GN NNNNTNCC

GNN N GGA TT NTT

Left

Slow Tidal wind

Signal G:104 A:448 T:303 C:232
DT 4%Ac[A Set-AnyPrimer]
SN 95080645
Points 1014, 11000

Page 1 of 2

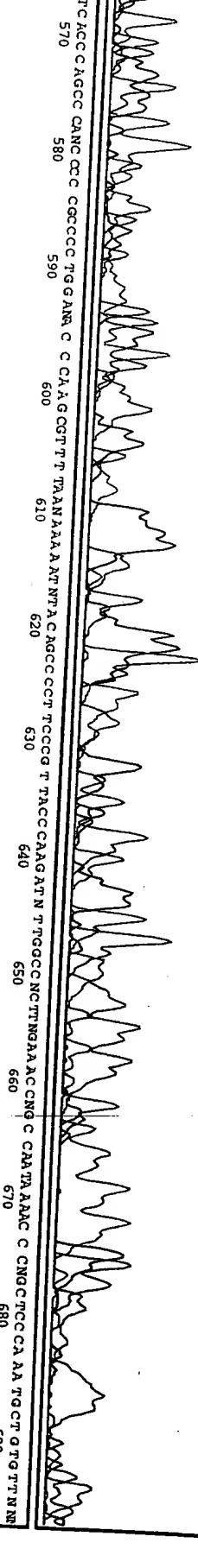
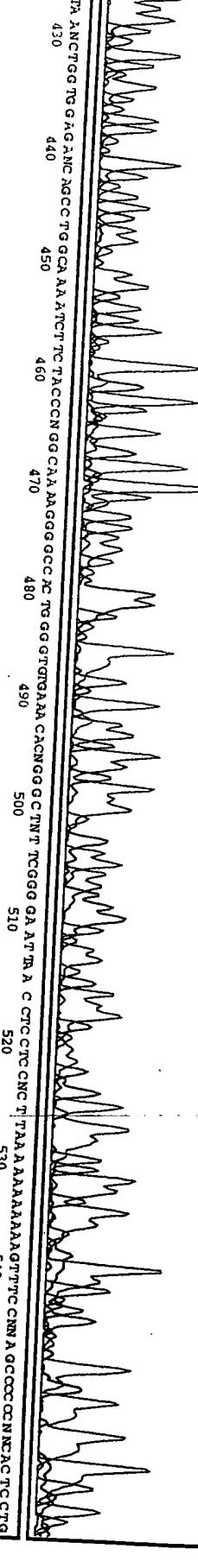
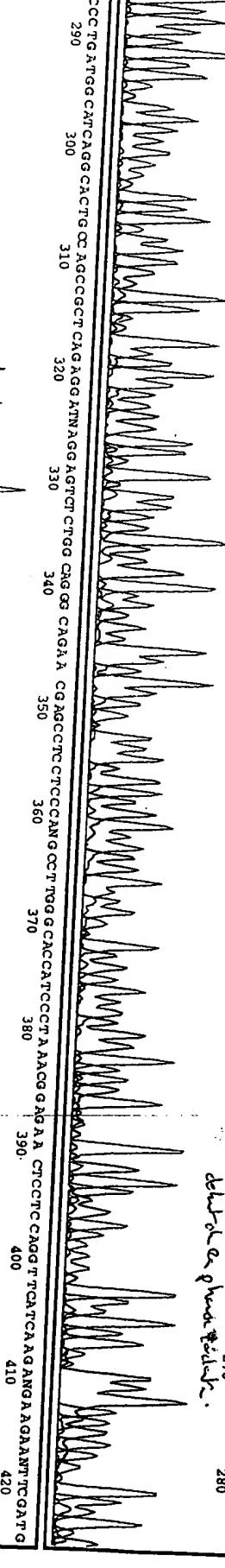
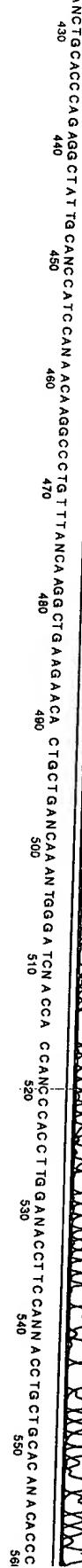
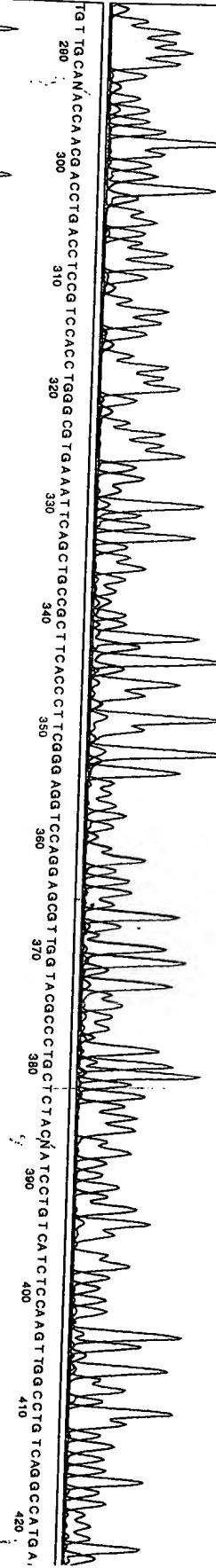
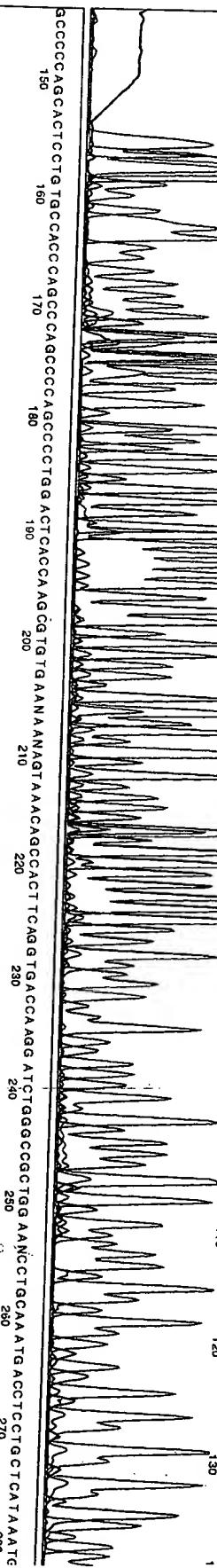


Figure 1. A typical example of a noisy signal recorded from a single neuron.

Signal G:265 A:609 T:272 C:286
*D14%AcA Set-AnyPrimer)
SN 95080645
Points 1203 to 11812 Base 1 to 203

Spacing: 11.70 ABI100

Page



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570 580 590 600 610 620 630 640 650 660 670 680

**ABI
PRISM**

Model 377
Version 2.1.1

20•CM 3
CM 3
Lane 20

Signal G:4B3 A:1087 T:367 C:416
*D14%Ac(A Sat-AnyPrimer)
S/N 9508045
Points 1209 to 11812 Base 1: 1209

Spacng: 11.29 ABT100

Page 1 of 2

